ABSTRACT

The present invention generally relates to a MHC ligand database

populated with MHC ligand sequences, motifs, extended motifs, submotifs,

ligands unique to infected cells, tumor specific ligands, as well as a collection

of current and future developed MHC ligand sequences developed by

alternative methods. Other than the ligand sequences developed by

alternative methods (which are in many cases non-standardized), the

remaining ligand sequences are obtained in a standardized and minimum-

variable dependent manner from soluble HLA molecules constructed

according to the methodology described herein. The present invention

further includes methodologies incorporating linear and predictive algorithm

searching and comparison utilities.